

21415-0015US.txt

<110> Ian Hector Frazer
 <120> A method for optimising gene expression using synonymous codon optimisation
 <130> 21415-0015US
 <140> USSN 10/534,130
 <141> 2005-05-06
 <150> PCT/AU2003/001487
 <151> 2003-11-10
 <150> USSN 60/425,163
 <151> 2002-11-08
 <160> 126
 <170> PatentIn version 3.2
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 agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg gaa 48
 Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 1 5 10 15
 ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag ggt 96
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 20 25 30
 gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc acc 144
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 35 40 45
 act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc tct 192
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
 50 55 60
 tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag cat 240
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
 65 70 75 80
 gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga acc 288
 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 85 90 95
 atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc aag 336
 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 100 105 110

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ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att gac	384
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp	
115 120 125	
ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac tat	432
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr	
130 135 140	
aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc atc	480
Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile	
145 150 155 160	
aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg cag	528
Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln	
165 170 175	
ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct gtg	576
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val	
180 185 190	
ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct aaa	624
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys	
195 200 205	
gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg acc	672
Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr	
210 215 220	
gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga	714
Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	
225 230 235	

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Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 1 5 10 15

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 20 25 30

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 35 40 45

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser
 50 55 60

Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His
 65 70 75 80

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 85 90 95

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 100 105 110

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 115 120 125

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 130 135 140

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 145 150 155 160

Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
 165 170 175

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 180 185 190

Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys
 195 200 205

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
 210 215 220

Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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<400> 16

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Arg Arg Arg Arg Arg Arg
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<400> 22

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Asp Asp Asp Asp Asp Asp
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Asp Asp Asp Asp Asp Asp
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<220>
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 Cys Cys Cys Cys Cys Cys
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gaa gaa gaa gaa gaa gaa
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Glu Glu Glu Glu Glu Glu
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gag gag gag gag gag gag
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Glu Glu Glu Glu Glu Glu
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<221> CDS

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<212> PRT

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<223> Gly(GGA)x6

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Gly Gly Gly Gly Gly Gly
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<223> Gly(GGG)x6

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 Gly Gly Gly Gly Gly Gly
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 Gly Gly Gly Gly Gly Gly
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 His His His His His His
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His His His His His His
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 His His His His His His
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His His His His His His
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Ile Ile Ile Ile Ile Ile
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ile ile ile ile ile ile
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ile ile ile ile ile ile
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ctc ctc ctc ctc ctc ctc
Leu Leu Leu Leu Leu Leu
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Leu Leu Leu Leu Leu Leu
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ttg ttg ttg ttg ttg ttg
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 cta cta cta cta cta cta
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<400> 70

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<220>
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 1 5

18

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<220>
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<400> 72

Leu Leu Leu Leu Leu Leu
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<210> 73
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<212> DNA
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<220>
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<220>
 <221> CDS
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 aag aag aag aag aag aag
 Lys Lys Lys Lys Lys Lys
 1 5

18

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<400> 74

Lys Lys Lys Lys Lys Lys
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<210> 75
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<220>
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<400> 75
 aaa aaa aaa aaa aaa aaa
 Lys Lys Lys Lys Lys Lys
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 <212> PRT
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<220>
 <223> Lys(AAA)x6

<400> 76

Lys Lys Lys Lys Lys Lys
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<220>
 <221> CDS
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 Phe Phe Phe Phe Phe Phe
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<220>
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<400> 78

Phe Phe Phe Phe Phe Phe
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<220>
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<220>
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Phe Phe Phe Phe Phe Phe
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ccc ccc ccc ccc ccc ccc
Pro Pro Pro Pro Pro Pro
1 5

18

<210> 82
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48

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 Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro Ser Ile Ser Thr Ser
 20 25 30

96

gaa atc gga gac act gag gat gcc ctt cag cag gtg gag gag att ggc
 Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln Val Glu Glu Ile Gly
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144

ata gag aag gca gcc atg gac atg acc gtc ttc ctg aag ctg cag aag
 Ile Glu Lys Ala Ala Met Asp Met Thr Val Phe Leu Lys Leu Gln Lys
 50 55 60

192

aga gtg cgc gaa ctt gag cag gag agg aag aag ctg cag gcg cag cta
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240

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Cys 385	Leu	Pro	Ala	Tyr	Ile 390	Leu	Tyr	Met	Cys	Ile 395	Arg	His	Ala	Asp	Tyr 400		
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Thr	Asn	Asp	Asp	Leu 405	Lys	Val	His	Ser	Leu 410	Leu	Ser	Ser	Thr	Ile 415	Asn		
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 625 630 635 640

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 Page 37

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 180 185 190
 Met Glu Pro Asn Ile Asn Ala Arg Thr Ser Trp Pro Asn Ser Glu Lys
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 Thr Asn Asp Asp Leu Lys Val His Ser Leu Leu Ser Ser Thr Ile Asn
 405 410 415
 Gly Ile Lys Lys Val Leu Lys Lys His Asn Asp Asp Phe Glu Met Thr
 420 425 430
 Ser Phe Trp Leu Ser Asn Thr Cys Arg Phe Leu His Cys Leu Lys Gln
 435 440 445
 Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln Asn Ile Ala Lys Gln Asn
 450 455 460
 Glu His Cys Leu Lys Asn Phe Asp Leu Thr Glu Tyr Arg Gln Val Leu
 465 470 475 480
 Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln Leu Ile Lys Met Pro Glu
 485 490 495
 Gly Leu Leu Gln Pro Met Ile Val Ser Ala Met Leu Glu Asn Glu Ser
 500 505 510

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Ile Gln Gly Leu Ser Gly Val Arg Pro Thr Gly Tyr Arg Lys Arg Ser
515 520 525

Ser Ser Met Val Asp Gly Glu Asn Ser Phe His Thr Val Leu Cys Asp
530 535 540

Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln Leu Phe
545 550 555 560

Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg Lys Asp
565 570 575

Ala Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile Ser Gln
580 585 590

Leu Glu Glu Trp Leu Arg Gly Lys Asn Leu His Gln Ser Gly Ala Val
595 600 605

Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln Leu Lys
610 615 620

Lys Lys Thr His Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys Thr Ser
625 630 635 640

Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr Pro Leu
645 650 655

Asn Glu Phe Glu Glu Arg Val Thr Val Ser Phe Ile Arg Thr Ile Gln
660 665 670

Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu Asp Ser
675 680 685

Lys His Val Phe Pro Val Leu Phe Pro Tyr Asn Pro Ser Ala Leu Thr
690 695 700

Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe Leu Asn
705 710 715 720

Glu Val

<210> 123
<211> 549
<212> DNA
<213> Artificial Sequence

<220>

<223> BAR gene

<220>

<221> CDS

<222> (1)..(549)

<400> 123

agc	cca	gaa	cga	cgc	ccg	gcc	gac	atc	cgc	cgt	gcc	acc	gag	gcg	gac	48
Ser	Pro	Glu	Arg	Arg	Pro	Ala	Asp	Ile	Arg	Arg	Ala	Thr	Glu	Ala	Asp	
1				5					10					15		

atg	ccg	gcg	gtc	tgc	acc	atc	gtc	aac	cac	tac	atc	gag	aca	agc	acg	96
Met	Pro	Ala	Val	Cys	Thr	Ile	Val	Asn	His	Tyr	Ile	Glu	Thr	Ser	Thr	
			20					25					30			

gtc	aac	ttc	cgt	acc	gag	ccg	cag	gaa	ccg	cag	gag	tgg	acg	gac	gac	144
Val	Asn	Phe	Arg	Thr	Glu	Pro	Gln	Glu	Pro	Gln	Glu	Trp	Thr	Asp	Asp	
		35					40					45				

ctc	gtc	cgt	ctg	cgg	gag	cgc	tat	ccc	tgg	ctc	gtc	gcc	gag	gtg	gac	192
Leu	Val	Arg	Leu	Arg	Glu	Arg	Tyr	Pro	Trp	Leu	Val	Ala	Glu	Val	Asp	
	50					55					60					

ggc	gag	gtc	gcc	ggc	atc	gcc	tac	gcg	ggc	ccc	tgg	aag	gca	cgc	aac	240
Gly	Glu	Val	Ala	Gly	Ile	Ala	Tyr	Ala	Gly	Pro	Trp	Lys	Ala	Arg	Asn	
65				70					75						80	

gcc	tac	gac	tgg	acg	gcc	gag	tcg	acc	gtg	tac	gtc	tcc	ccc	cgc	cac	288
Ala	Tyr	Asp	Trp	Thr	Ala	Glu	Ser	Thr	Val	Tyr	Val	Ser	Pro	Arg	His	
				85					90					95		

cag	cgg	acg	gga	ctg	ggc	tcc	acg	ctc	tac	acc	cac	ctg	ctg	aag	tcc	336
Gln	Arg	Thr	Gly	Leu	Gly	Ser	Thr	Leu	Tyr	Thr	His	Leu	Leu	Lys	Ser	
			100					105					110			

ctg	gag	gca	cag	ggc	ttc	aag	agc	gtg	gtc	gct	gtc	atc	ggg	ctg	ccc	384
Leu	Glu	Ala	Gln	Gly	Phe	Lys	Ser	Val	Val	Ala	Val	Ile	Gly	Leu	Pro	
		115					120					125				

aac	gac	ccg	agc	gtg	cgc	atg	cac	gag	gcg	ctc	gga	tat	gcc	ccc	cgc	432
Asn	Asp	Pro	Ser	Val	Arg	Met	His	Glu	Ala	Leu	Gly	Tyr	Ala	Pro	Arg	
	130					135					140					

ggc	atg	ctg	cgg	gcg	gcc	ggc	ttc	aag	cac	ggg	aac	tgg	cat	gac	gtg	480
Gly	Met	Leu	Arg	Ala	Ala	Gly	Phe	Lys	His	Gly	Asn	Trp	His	Asp	Val	
145				150						155					160	

ggt	ttc	tgg	cag	ctg	gac	ttc	agc	ctg	ccg	gtg	ccg	ccc	cgt	ccg	gtc	528
Gly	Phe	Trp	Gln	Leu	Asp	Phe	Ser	Leu	Pro	Val	Pro	Pro	Arg	Pro	Val	
				165					170					175		

ctg	ccc	gtc	acc	gaa	atc	tga										549
Leu	Pro	Val	Thr	Glu	Ile											
			180													

<210> 124

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> BAR gene

<400> 124

Ser Pro Glu Arg Arg Pro Ala Asp Ile Arg Arg Ala Thr Glu Ala Asp
 1 5 10 15

Met Pro Ala Val Cys Thr Ile Val Asn His Tyr Ile Glu Thr Ser Thr
 20 25 30

Val Asn Phe Arg Thr Glu Pro Gln Glu Pro Gln Glu Trp Thr Asp Asp
 35 40 45

Leu Val Arg Leu Arg Glu Arg Tyr Pro Trp Leu Val Ala Glu Val Asp
 50 55 60

Gly Glu Val Ala Gly Ile Ala Tyr Ala Gly Pro Trp Lys Ala Arg Asn
 65 70 75 80

Ala Tyr Asp Trp Thr Ala Glu Ser Thr Val Tyr Val Ser Pro Arg His
 85 90 95

Gln Arg Thr Gly Leu Gly Ser Thr Leu Tyr Thr His Leu Leu Lys Ser
 100 105 110

Leu Glu Ala Gln Gly Phe Lys Ser Val Val Ala Val Ile Gly Leu Pro
 115 120 125

Asn Asp Pro Ser Val Arg Met His Glu Ala Leu Gly Tyr Ala Pro Arg
 130 135 140

Gly Met Leu Arg Ala Ala Gly Phe Lys His Gly Asn Trp His Asp Val
 145 150 155 160

Gly Phe Trp Gln Leu Asp Phe Ser Leu Pro Val Pro Pro Arg Pro Val
 165 170 175

Leu Pro Val Thr Glu Ile
 180

<210> 125

<211> 366

<212> DNA

<213> Human

<220>

<221> CDS

<222> (1)..(363)

<400> 125

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atg gga aaa ggt gtg aaa tcc ccg ggg gag aag tca cgc tat gag acc 48
Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr
1 5 10 15

tca ctg aat ctg acc acc aag cgc ttc ctg gag ctg ctg agc cac tcg 96
Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser
20 25 30

gct gac ggt gtc gtc gac ctg aac tgg gct gcc gag gtg ctg aag gtg 144
Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val
35 40 45

cag aag cgg cgc atc tat gac atc acc aac gtc ctt gag ggc atc cag 192
Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln
50 55 60

ctc att gcc aag aag tcc aag aac cac atc cag tgg ctg ggc agc cac 240
Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His
65 70 75 80

acc aca gtg ggc gtc ggc gga cgg ctt gag ggg ttg acc cag gac ctc 288
Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu
85 90 95

cga cag ctg cag gag agc gag cag cag ctg gac cac ctg atg aat atc 336
Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile
100 105 110

tgt act acg cag ctg cgc ctg ctc tcc tga 366
Cys Thr Thr Gln Leu Arg Leu Leu Ser
115 120

<210> 126
<211> 121
<212> PRT
<213> Human

<400> 126

Met Gly Lys Gly Val Lys Ser Pro Gly Glu Lys Ser Arg Tyr Glu Thr 15
1 5 10

Ser Leu Asn Leu Thr Thr Lys Arg Phe Leu Glu Leu Leu Ser His Ser 30
20 25

Ala Asp Gly Val Val Asp Leu Asn Trp Ala Ala Glu Val Leu Lys Val 45
35 40

Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu Gly Ile Gln 60
50 55

Leu Ile Ala Lys Lys Ser Lys Asn His Ile Gln Trp Leu Gly Ser His 80
65 70 75

Thr Thr Val Gly Val Gly Gly Arg Leu Glu Gly Leu Thr Gln Asp Leu 95
85 90

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Arg Gln Leu Gln Glu Ser Glu Gln Gln Leu Asp His Leu Met Asn Ile
100 105 110

Cys Thr Thr Gln Leu Arg Leu Leu Ser
115 120